



# SEQUENCE LISTING

<110> Anderson, John P.  
Basi, Gurigbal  
Doane, Minh Tam  
Frigon, Normand  
John, Varghese  
Power, Michael  
Sinha, Sukanto  
Tatsuno, Gwen  
Tung, Jay  
Wang, Shuwen  
McConlogue, Lisa

<120> Beta-Secretase Enzyme Compositions and  
Methods

<130> 228-US-NEWC1

<140> 09/723,722

<141> 2000-11-28

<150> US 09/501,708

<151> 2000-02-10

<150> 60/119,571

<151> 1999-02-10

<150> 60/139,172

<151> 1999-06-15

<160> 104

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 1

atggcccaag	ccctgcccctg	gtccctgctg	tggatgggcg	cgggagtget	gcctgcccac	60
ggcaccacgc	acggcatccg	gtgcccctg	cgcagcggcc	tggggggcgc	ccccctgggg	120
ctgcggtctg	cccgggagac	cgacgaagag	cccgaggagc	ccggccggag	gggcagcttt	180
gtggagatgg	tggacaacct	gaggggcaag	tcggggcagg	gctactacgt	ggagatgacc	240
gtgggcagcc	ccccgcagac	gctcaacatc	ctgggtggata	caggcagcag	taactttgca	300
gtgggtgctg	ccccccaccc	cttctgcat	cgctactacc	agaggcagct	gtccagcaca	360
taccgggacc	tccggaagg	tgtgtatgtg	ccctacaccc	agggcaagt	ggaaggggag	420
ctgggcaccg	acctggtaag	catcccccat	ggccccaacg	tcactgtgcg	tgccaacatt	480
gctgccatca	ctgaatcaga	caagttcttc	atcaacggct	ccaactggga	aggcatcctg	540
gggctggcct	atgctgagat	tgcaggcct	gacgactccc	tggagccttt	ctttgactct	600
ctggtaaaag	agaccacgt	tcccaacctc	ttctccctgc	agctttgtgg	tgctggcttc	660
cccctcaacc	agtctgaagt	gctggcctct	gtcggaggga	gcatgatcat	tggaggatc	720
gaccactcgc	tgtacacagg	cagtctctgg	tatacaccca	tccggcgggg	gtgggtattat	780
gagggtgatca	ttgtgcgggt	ggagatcaat	ggacaggatc	tgaaaatgga	ctgcaaggag	840
tacaactatg	acaagagcat	tgtggacagt	ggcaccacca	accttcgttt	gccaagaaa	900
gtgtttgaag	ctgcagtcaa	atccatcaag	gcagcctcct	ccacggagaa	gttccctgat	960
ggtttctggc	taggagagca	gctgggtgtg	tggcaagcag	gcaccacccc	ttggaacatt	1020
ttcccagtca	tctcactcta	cctaattgggt	gaggttacca	accagtcctt	ccgcatcacc	1080
atccttccgc	agcaatacct	gcggccagtg	gaagatgtgg	ccacgtccca	agacgactgt	1140

tacaagtttg	ccatctcaca	gtcatccacg	ggcactgtta	tgggagctgt	tatcatggag	1200
ggcttctacg	ttgtctttga	tcgggcccgga	aaacgaattg	gctttgctgt	cagcgcttgc	1260
catgtgcacg	atgagttcag	gacggcagcg	gtggaaggcc	cttttgtcac	cttggacatg	1320
gaagactgtg	gctacaacat	tccacagaca	gatgagtcaa	ccctcatgac	catagcctat	1380
gtcatggctg	ccatctgcgc	cctcttcacg	ctgccactct	gcctcatggt	gtgtcagtgg	1440
cgctgcctcc	gctgcctgcg	ccagcagcat	gatgactttg	ctgatgacat	ctccctgctg	1500
aag						1503

<210> 2

<211> 501

<212> PRT

<213> Homo sapiens

<400> 2

Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val
1				5					10					15	
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
			20					25					30		
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70					75					80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
			100					105					110		
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
		115					120					125			
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130					135					140				
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145					150					155					160
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
				165					170					175	
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
			180					185					190		
Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro
	195						200					205			
Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln
	210					215					220				
Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile
225					230					235					240
Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg
			245						250					255	
Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln
			260					265					270		
Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val
	275						280					285			
Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala
	290					295					300				
Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp
305					310					315					320
Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr
			325						330					335	
Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val
			340					345					350		
Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg
	355						360					365			

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
 370 375 380  
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
 385 390 395 400  
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
 405 410 415  
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
 420 425 430  
 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
 435 440 445  
 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala  
 450 455 460  
 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp  
 465 470 475 480  
 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp  
 485 490 495  
 Ile Ser Leu Leu Lys  
 500

<210> 3  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 gagagacgar garccwgagg agcc

24

<210> 4  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
 ID NO: 2

<400> 4  
 gagagacgar garccwgaag agcc

24

<210> 5  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
 ID NO: 2

<400> 5  
 gagagacgar garccwgaag aacc

24

<210> 6  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
 ID NO: 2

<400> 6

gagagacgar garccwgagg aacc	24
<210> 7	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Degenerate oligonucleotide primer derived from SEQ ID NO: 2	
<400> 7	
agagacgarg arccsgagga gcc	23
<210> 8	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Degenerate oligonucleotide primer derived from SEQ ID NO: 2	
<400> 8	
agagacgarg arccsgaaga gcc	23
<210> 9	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Degenerate oligonucleotide primer derived from SEQ ID NO: 2	
<400> 9	
agagacgarg arccsgaaga acc	23
<210> 10	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Degenerate oligonucleotide primer derived from SEQ ID NO: 2	
<400> 10	
agagacgarg arccsgagga acc	23
<210> 11	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Degenerate oligonucleotide primer derived from SEQ ID NO: 2	
<400> 11	
cgtcacagrt trtcaaccat etc	23

<210> 12  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
         ID NO: 2  
  
 <400> 12  
 cgtcacagrt trtctaccat ctc 23  
  
 <210> 13  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
         ID NO: 2  
  
 <400> 13  
 cgtcacagrt trtccaccat ctc 23  
  
 <210> 14  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
         ID NO: 2  
  
 <400> 14  
 cgtcacagrt trtcgaccat ctc 23  
  
 <210> 15  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
         ID NO: 2  
  
 <400> 15  
 cgtcacagrt trtcaaccat ttc 23  
  
 <210> 16  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
         ID NO: 2  
  
 <400> 16  
 cgtcacagrt trtctaccat ttc 23

<210> 17  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
       ID NO: 2  
  
 <400> 17  
 cgtcacagrt trtccaccat ttc 23  
  
 <210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
       ID NO: 2  
  
 <400> 18  
 cgtcacagrt trtcgaccat ttc 23  
  
 <210> 19  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
       ID NO: 2  
  
 <400> 19  
 gaggggcagc tttgtggaga 20  
  
 <210> 20  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
       ID NO: 2  
  
 <400> 20  
 cagcataggc cagccccagg atgcct 26  
  
 <210> 21  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
       ID NO: 2  
  
 <400> 21  
 gtgatggcag caatgttggc acgc 24

<210> 22  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<220>  
<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 22  
gaygargagc cngagga

17

<210> 23  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<220>  
<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 23  
gaygargagc cngaaga

17

<210> 24  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<220>  
<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 24  
gaygargaac cngagga

17

<210> 25  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<220>  
<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 25  
 gaygargaac cngaaga 17  
  
 <210> 26  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(15)  
 <223> n = A,T,C or G  
  
 <400> 26  
 rtttrtcnacc atttc 15  
  
 <210> 27  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(15)  
 <223> n = A,T,C or G  
  
 <400> 27  
 rtttrtcnacc atctc 15  
  
 <210> 28  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(17)  
 <223> n = A,T,C or G  
  
 <400> 28  
 tcnaccatyt cnacaaa 17  
  
 <210> 29  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <220>  
 <221> misc\_feature



<222> (1)...(17)  
 <223> n = A,T,C or G  
  
 <400> 29  
 tcnaccatyt cnacgaa 17  
  
 <210> 30  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 30  
 atattctaga gaygargagc cagaaga 27  
  
 <210> 31  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 31  
 atattctaga gaygargagc cggaaga 27  
  
 <210> 32  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 32  
 atattctaga gaygargagc ccgaaga 27  
  
 <210> 33  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 33  
 atattctaga gaygargagc ctgaaga 27  
  
 <210> 34  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(30)

<223> n = A,T,C or G

<400> 34  
acacgaattc ttrtcnacca tytcaacaaa 30

<210> 35  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<220>  
<221> misc\_feature  
<222> (1)...(30)  
<223> n = A,T,C or G

<400> 35  
acacgaattc ttrtcnacca tytcgacaaa 30

<210> 36  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<220>  
<221> misc\_feature  
<222> (1)...(30)  
<223> n = A,T,C or G

<400> 36  
acacgaattc ttrtcnacca tytccacaaa 30

<210> 37  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<220>  
<221> misc\_feature  
<222> (1)...(30)  
<223> n = A,T,C or G

<400> 37  
acacgaattc ttrtcnacca tytctacaaa 30

<210> 38  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<400> 38  
 aagagcccgg ccggaggggc a 21

<210> 39  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer

<400> 39  
 aaagctgccc ctccggccgg g 21

<210> 40  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer

<400> 40  
 agctcgttta gtgaaccgtc agatcg 26

<210> 41  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer

<400> 41  
 acctacaggt ggggtctttc attccc 26

<210> 42  
 <211> 1368  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
 gagaccgacg aagagcccga ggagcccggc cggaggggca gctttgtgga gatggtggac 60  
 aacctgaggg gcaagtcggg gcagggtac tacgtggaga tgaccgtggg cagccccccg 120  
 cagacgctca acatcctggg ggatacaggc agcagtaact ttgcagtggg tgctgcccc 180  
 ccccccttc tgcacgcta ctaccagagg cagctgtcca gcacataccg ggacctccgg 240  
 aagggtgtgt atgtgcccta caccagggc aagtgggaag gggagctggg caccgacctg 300  
 gtaagcatcc cccatggccc caacgtcact gtgcgtgcc aattgctgc catcactgaa 360  
 tcagacaagt tcttcatcaa cggctccaac tgggaaggca tcctggggct ggcctatgct 420  
 gagattgcca ggcctgacga ctccctggag cctttctttg actctctggt aaagcagacc 480  
 cacgttccca acctcttctc cctgcagctt tgtggtgctg gcttccccct caaccagtct 540  
 gaagtgctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctgcgtgtac 600

```

acaggcagtc tctggtatac acccatccgg cgggagtggg attatgaggt gatcattgtg      660
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag      720
agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca      780
gtcaaatacca tcaaggcagc ctctccacg gagaagttcc ctgatggttt ctggctagga      840
gagcagctgg tgtgctggca agcaggcacc accccttggg acattttccc agtcatctca      900
ctctacctaa tgggtgaggt taccaaccag tccttcgca tcaccatcct tccgcagcaa      960
tacctgcggc cagtgaaga tgtggccacg tccaagacg actgttacia gtttgccatc     1020
tcacagtcac ccacgggcac tgttatggga gctgttatca tggagggtt ctacgttgtc     1080
tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag     1140
ttcaggacgg cagcgggtga aggccctttt gtcaccttgg acatggaaga ctgtggctac     1200
aacattccac agacagatga gtcaaccctc atgaccatag cctatgtcat ggctgccatc     1260
tgcgccctct tcatgctgcc actctgcctc atggtgtgtc agtggcgctg cctccgctgc     1320
ctgcgccagc agcatgatga ctttgcctgat gacatctccc tgctgaag                    1368

```

```

<210> 43
<211> 456
<212> PRT
<213> Homo sapiens

```

```

<400> 43
Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1          5          10          15
Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
 20        25        30
Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
 35        40        45
Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
 50        55        60
His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
 65        70        75        80
Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
 85        90        95
Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
100       105       110
Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
115       120       125
Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
130       135       140
Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
145       150       155       160
His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
165       170       175
Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
180       185       190
Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
195       200       205

```

Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile
210						215					220				
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys
225					230					235					240
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val
				245					250					255	
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys
			260					265					270		
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala
		275					280					285			
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met
	290					295					300				
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln
305				310						315					320
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr
			325					330						335	
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val
		340						345					350		
Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile
		355					360					365			
Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala
	370					375					380				
Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr
385				390						395					400
Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val
			405					410						415	
Met	Ala	Ala	Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val
		420						425					430		
Cys	Gln	Trp	Arg	Cys	Leu	Arg	Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe
		435					440					445			
Ala	Asp	Asp	Ile	Ser	Leu	Leu	Lys								
450							455								

<210> 44  
 <211> 2348  
 <212> DNA  
 <213> Homo sapiens

<400> 44

ccatgccggc	ccctcacagc	cccgcgggga	gcccagagccc	gctgcccagg	ctggccgccc	60
ccgtgccgat	gtagcgggct	ccggatccca	gcctctcccc	tgctcccgtg	ctctgcggat	120
ctcccctgac	cgctctccac	agcccggacc	cgggggctgg	cccagggccc	tgcaggccct	180
ggcgtcctga	tgcccccaag	ctccctctcc	tgagaagcca	ccagcaccac	ccagacttgg	240
gggcaggcgc	cagggacgga	cgtgggccag	tgcgagccca	gagggcccga	aggccggggc	300
ccaccatggc	ccaagccctg	ccctggctcc	tgctgtggat	gggcgcggga	gtgctgcctg	360
cccacggcac	ccagcacggc	atccggctgc	ccctgcgcag	cggcctgggg	ggcgcccccc	420
tggggctgcy	gctgccccgg	gagaccgacg	aagagcccga	ggagcccggc	cggaggggca	480
gctttgtgga	gatggtggac	aacctgaggg	gcaagtccgg	gcagggctac	tacgtggaga	540
tgaccgtggg	cagccccccg	cagacgctca	acatcctggt	ggatacaggc	agcagtaact	600
ttgcagtggg	tgctgcccc	cacccttcc	tgcacgcta	ctaccagagg	cagctgtcca	660
gcacataccg	ggacctccgg	aagggtgtgt	atgtgcccta	caccagggc	aagtgggaag	720
gggagctggg	caccgacctg	gtaagcatcc	cccatggccc	caacgtcact	gtgcgtgcca	780
acattgctgc	catcactgaa	tcagacaagt	tcttcatcaa	cggctccaac	tggaagggca	840
tcctgggggt	ggcctatgct	gagattgcca	ggcctgacga	ctccctggag	cctttctttg	900
actctctggt	aaagcagacc	cacgttccca	acctcttctc	cctgcagctt	tgtggtgctg	960
gcttccccct	caaccagtct	gaagtgtgtg	cctctgtcgg	agggagcatg	atcattggag	1020
gtatcgacca	ctcgtgttac	acaggcagtc	tctggtatac	acccatccgg	cgggagtggg	1080
attatgaggt	gatcattgtg	cgggtggaga	tcaatggaca	ggatctgaaa	atggactgca	1140
aggagtacaa	ctatgacaag	agcattgtgg	acagtggcac	caccaacctt	cgtttgcccc	1200
agaaagtgtt	tgaagctgca	gtcaaatacca	tcaaggcagc	ctcctccacg	gagaagttcc	1260
ctgatggttt	ctggctagga	gagcagctgg	tgtgctggca	agcaggcacc	accccttgga	1320

```

acattttccc agtcattctca ctctaccta tgggtgaggt taccaaccag tccttccgca 1380
tcaccatcct tccgcagcaa tacctgcggc cagtggaga tgtggccacg tcccaagacg 1440
actgttacaa gtttgccatc tcacagtcac ccacgggcac tgttatggga gctgttatca 1500
tggagggtct ctacgttgtc tttgatcggg cccgaaaacg aattggcttt gctgtcagcg 1560
cttgccatgt gcacgatgag ttcaggacgg cagcgggtga aggccctttt gtcaccttgg 1620
acatggaaga ctgtggctac aacattccac agacagatga gtcaaccctc atgaccatag 1680
cctatgtcat ggctgccatc tgcgccctct tcatgctgcc actctgcctc atgggtgtgtc 1740
agtggcgctg cctccgctgc ctgcgccagc agcatgatga ctttgctgat gacatctccc 1800
tgctgaagtg aggaggccca tgggcagaag atagagattc ccctggacca cacctccgtg 1860
gttcactttg gtcacaagta ggagacacag atggcacctg tggccagagc acctcaggac 1920
cctccccacc caccaaatgc ctctgccttg atggagaagg aaaaggctgg caagggtgggt 1980
tccagggtact gtacctgtag gaaacagaaa agagaagaaa gaagcactct gctggcgagg 2040
atactcttgg tcacctcaaa ttttaagtcgg gaaattctgc tgcttgaaac ttcagccctg 2100
aacctttgtc caccattcct ttaaattctc caacccaaag tattcttctt ttcttagttt 2160
cagaagtact ggcattcacac gcagggtacc ttggcgtgtg tccctgtggg accctggcag 2220
agaagagacc aagcttgttt ccctgctggc caaagtcagt aggagaggat gcacagtttg 2280
ctatttgctt tagagacagg gactgtataa acaagcctaa cattggtgca aagattgcct 2340
cttgaatt

```

```

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Flag sequence

```

```

<400> 45
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

```

```

<210> 46
<211> 21
<212> PRT
<213> Homo sapiens

```

```

<400> 46
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15
Leu Pro Ala His Gly
20

```

```

<210> 47
<211> 24
<212> PRT
<213> Homo sapiens

```

```

<400> 47
Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15
Pro Leu Gly Leu Arg Leu Pro Arg
20

```

```

<210> 48
<211> 16080
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Expression Vector pCEK

```

<220>  
 <221> misc\_feature  
 <222> (1)...(16080)  
 <223> n = A,T,C or G

<400> 48

ttctcatggt	tgacagctta	tcatcgcaga	tccgggcaac	gttggtgcat	tgctgcaggc	60
gcagaactgg	taggtatgga	agatccgatg	tacgggccag	atatacgcgt	tgacattgat	120
tattgactag	ttattaatag	taatcaatta	cggggtcatt	agttcatagc	ccatatatgg	180
agttccgcgt	tacataactt	acggtaaatg	gcccgctgg	ctgaccgccc	aacgaccccc	240
gcccattgac	gtcaataatg	acgtatgttc	ccatagtaac	gccaataggg	actttccatt	300
gacgtcaatg	ggtggactat	ttacggtaaa	ctgcccactt	ggcagtacat	caagtgtatc	360
atatgccaa	tacgccccct	attgacgtca	atgacggtaa	atggcccgcg	tggcattatg	420
cccagtacat	gaccttatgg	gactttccta	cttggcagta	catctacgta	ttagtcatcg	480
ctattaccat	ggtgatgcgg	ttttggcagt	acatcaatgg	gcgtggatag	cggtttgact	540
cacggggatt	tccaagtctc	caccccatgg	acgtcaatgg	gagtttgttt	tggcaccaaaa	600
atcaacggga	ctttccaaaa	tgtcgttaaca	actccgcccc	attgacgcaa	atgggcggta	660
ggcgtgtacg	gtggggaggtc	tatataagca	gagctctctg	gctaactaga	gaacccactg	720
cttactggct	tatcgaaatt	aatacgactc	actataggga	gacccaagct	ctgttgggct	780
cgcggttgag	gacaaaactct	tcgcggtctt	tccagtactc	ttggatcgga	aaccgctcgg	840
cctccgaacg	gtactccgcc	accgaggggac	ctgagcgagt	ccgcatcgac	cggatcggaa	900
aacctctcga	ctgttggggt	gagtactccc	tctcaaaagc	gggcatgact	tctgcgctaa	960
gattgtcagt	ttccaaaaac	gaggaggatt	tgatattcac	ctggcccgcg	gtgatgcctt	1020
tgaggggtgg	cgcgtccatc	tggtcagaaa	agacaatctt	tttgttgtca	agcttgagggt	1080
gtggcaggct	tgagatctgg	ccatacactt	gagtgacaat	gacatccact	ttgcctttct	1140
ctccacaggt	gtccactccc	aggtccaact	gcaggtcgac	tctagaccgc	gggaattctg	1200
cagatatcca	tcacactggc	cgcactcgtc	cccagcccgc	ccgggagctg	cgaagccgca	1260
gctggattat	ggtggcctga	gcagccaacg	cagccgcagg	agcccggagc	ccttgcccct	1320
gcccgcgccg	cgccccgcgc	gggggaccag	ggaagccgcc	accggcccgc	catgcccgcc	1380
cctcccagcc	ccgcggggag	cccgcgcccg	ctgcccaggc	tggccgcgcg	cgtgccgatg	1440
tagcgggctc	cggatcccag	cctctcccct	gctcccgtgc	tctgcggatc	ttcccctgacc	1500
gctctccaca	gcccggaccc	gggggctggc	ccagggccct	gcaggccctg	gcgtcctgat	1560
gcccccaagc	tccctctcct	gagaagccac	cagcaccacc	cagacttggg	ggcaggcgcc	1620
agggacggac	gtggggccagt	gcgagcccag	agggcccga	ggccgggggc	caccatggcc	1680
caagccctgc	cctggctcct	gctgtggatg	ggcgcgggag	tgctgcctgc	ccacggcacc	1740
cagcacggga	tccggctgcc	cctgcgcagc	ggcctggggg	gcgccccctt	ggggctgcgg	1800
ctgccccggg	agaccgacga	agagcccag	gagccgggcc	ggaggggcag	ctttgtggag	1860
atggtggaca	acctgagggg	caagtccggg	cagggtact	acgtggagat	gaccgtgggc	1920
agccccccgc	agacgctcaa	catcctgggt	gatacaggca	gcagtaactt	tgcagtgggt	1980
gctgcccccc	accccttctt	gcacgctac	taccagaggc	agctgtccag	cacataaccg	2040
gacctccgga	aggggtgtgt	tgtgccctac	accaggggca	agtgggaagg	ggagctgggc	2100
accgacctgg	taagcatccc	ccatggcccc	aacgtcactg	tgcgtgccaa	cattgctgcc	2160
atcactgaat	cagacaagtt	cttcatcaac	ggctccaact	gggaaggcat	cctggggctg	2220
gcctatgctg	agattgccag	gcctgacgac	tccctggagc	ctttctttga	ctctctggta	2280
aagcagaccc	acgttcccaa	cctcttctcc	ctgcagcttt	gtggtgctgg	cttccccctc	2340
aaccagtctg	aagtgtctgg	ctctgtcgga	gggagcatga	tcattggagg	tatcgaccac	2400
tcgctgtaca	caggcagttc	ctggtataca	cccatccggc	gggagtggta	ttatgaggtc	2460
atcattgtgc	gggtggagat	caatggacag	gatctgaaaa	tggactgcaa	ggagtacaac	2520
tatgacaaga	gcattgtgga	cagtggcacc	accaaccttc	gtttgcccac	gaaagtgttt	2580
gaagctgcag	tcaaatccat	caaggcagcc	tcctccacgg	agaagttccc	tgatggtttc	2640
tggttaggag	agcagctggt	gtgctggcaa	gcaggcacca	ccccttggaa	cattttccca	2700
gtcatctcac	tctacctaat	gggtgagggt	accaaccagt	ccttcgcgat	caccatcctt	2760
ccgcagcaat	acctgcggcc	agtggaaagt	gtggccacgt	cccaagacga	ctgttacaag	2820
tttgccatct	cacagtcac	cacgggcact	gttatgggag	ctgttatcat	ggagggtctc	2880
tacgttgtct	ttgatcgggc	ccgaaaacga	attggctttg	ctgtcagcgc	ttgccatgtg	2940
cacgatgagt	tcaggacggc	agcgggtggaa	ggcccttttg	tcaccttggg	catggaagac	3000
tgtggctaca	acattccaca	gacagatgag	tcaaccttca	tgaccatagc	ctatgtcatg	3060
gctgccatct	gcgcccctct	catgctgcca	ctctgcctca	tgggtgtgtca	gtggcgctgc	3120
ctccgctgcc	tgcgccagca	gcattgatgac	tttgctgatg	acatctccct	gctgaagtga	3180
ggaggcccat	gggcagaaga	tagagattcc	cctggaccac	acctccgtgg	ttcacttttg	3240

tcacaagtag	gagacacaga	tggcacctgt	ggccagagca	cctcaggacc	ctccccaccc	3300
accaaagtgc	tctgccttga	tggagaagga	aaaggctggc	aaggtgggtt	ccagggactg	3360
tacctgtagg	aaacagaaaa	gagaagaaa	aagcactctg	ctggcgggaa	tactcttggg	3420
cacctcaa	ttaagtcggg	aaattctgct	gcttgaaact	tcagccctga	acctttgtcc	3480
accattcctt	taaattctcc	aacccaaagt	attcttcttt	tcttagtttc	agaagtactg	3540
gcatcacacg	caggttacct	tggcgtgtgt	ccctgtggta	ccctggcaga	gaagagacca	3600
agcttgtttc	cctgctggcc	aaagtcagta	ggagaggatg	cacagtttgc	tatttgcttt	3660
agagacaggg	actgtataaa	caagcctaac	attggtgcaa	agattgcctc	ttgaattaaa	3720
aaaaaaaa	agattgacta	tttatacaaa	tgggggcggc	tggaaagagg	agaaggagag	3780
ggagtacaaa	gacagggaat	agtgggatca	aagctagtaa	aggcagaaac	acaaccactc	3840
accagtcccta	gttttagacc	tcattctcaa	gatagcatcc	catctcagaa	gatgggtgtt	3900
gttttcaatg	ttttcttttc	tgtggttgca	gcctgaccaa	aagtgagatg	ggaagggtct	3960
atctagccaa	agagctcttt	tttagctctc	ttaaatgaag	tgccactaa	gaagttccac	4020
ttaacacatg	aatttctgcc	atattaattt	cattgtctct	atctgaacca	ccctttattc	4080
tacatatgat	aggcagcact	gaaatatcct	aaccccctaa	gctccagggt	ccctgtggga	4140
gagcaactgg	actatagcag	ggctgggctc	tgtcttctct	gtcataggct	cactctttcc	4200
cccaaatctt	cctctggagc	tttgcagcca	aggtgctaaa	aggaataggt	aggagacctc	4260
ttctatctaa	tccttaaaa	cataatgttg	aacattcatt	caacagctga	tgccctataa	4320
cccctgcctg	gatttcttcc	tattaggcta	taagaagtga	caagatcttt	acataattca	4380
gagtgggttc	attgccttcc	tacctctctc	aatggccctc	ccattttatt	gactaaagca	4440
tcacacagtg	gcactagcat	tataccaaga	gtatgagaaa	tacagtgtct	tatgggtcta	4500
acattactgc	cttcagtatc	aaggctgcct	ggagaaagga	tggcagcctc	agggtcttct	4560
tatgtcctcc	accacaagag	ctccttgatg	aaggtcatct	ttttcccta	tcctgttctt	4620
cccctccccg	ctcctaattg	taogtgggta	cccaggctgg	ttcttgggct	aggtagtggg	4680
gaccaagttc	attacctccc	tatcagttct	agcatagtaa	actacggtac	cagtgttagt	4740
gggaagagct	gggttttctc	agtataccca	ctgcaccta	ctcctacctg	gtcaacccgc	4800
tgcttccagg	tatgggacct	gctaagtgtg	gaattacctg	ataagggaga	gggaaataca	4860
aggagggtct	ctgggtgttc	tggcctcagc	cagctgcccc	caagccataa	accaataaaa	4920
caagaatact	gagtcagttt	tttatctggg	ttctcttcat	tccactgca	cttgggtctg	4980
ctttggctga	ctgggaacac	cccataacta	cagagtctga	caggaagact	ggagactgtc	5040
cacttctagc	tcggaactta	ctgtgtaaat	aaactttcag	aactgctacc	atgaagtga	5100
aatgccacat	tttgctttat	aatttctacc	catgttgagg	aaaactggct	ttttcccagc	5160
cctttccagg	gcataaaact	caaccccttc	gatagcaagt	cccatcagcc	tattattttt	5220
ttaaagaaaa	cttgcaactg	tttttctttt	tacagttact	tccttctctg	cccaaaatta	5280
taaactctaa	gtgtaaaaaa	aagtcttaac	aacagcttct	tgcttgtaaa	aatatgtatt	5340
atacatctgt	attttttaaa	tctgctcctg	aaaaatgact	gtcccattct	ccactcactg	5400
catttggggc	ctttcccat	ggtctgcctg	tcttttatca	ttgcaggcca	gtggacagag	5460
ggagaaggga	gaacaggggt	cgccaacact	tgtgttgctt	tctgactgat	cctggaacaag	5520
aaagagtaac	actgaggcgc	tcgctcccat	gcacaactct	ccaaaacact	tatcctcctg	5580
caagagtggg	ctttccgggt	ctttactggg	aagcagttaa	gccccctcct	caccccttcc	5640
ttttttcttt	ctttactcct	ttggcttcaa	aggattttgg	aaaagaaaca	atatgcttta	5700
cactcatttt	caatttctaa	atttgcaggg	gatactgaaa	aatacggcag	gtggcctaag	5760
gctgctgtaa	agttgagggg	agaggaaatc	ttaaagattac	aagataaaaa	acgaatcccc	5820
taaacaaaaa	gaacaataga	actgggtctc	cattttgcc	cctttcctgt	tcatgacagc	5880
tactaacctg	gagacagtaa	catttccatta	accaaagaaa	gtgggtcacc	tgacctctga	5940
agagctgagt	actcaggcca	ctccaatcac	ctacaagat	gccaaggagg	tcccagggaag	6000
tccagctcct	taaactgacg	ctagtcaata	aacctgggca	agtgaggcaa	gagaaatgag	6060
gaagaatcca	tctgtgaggt	gacaggcacg	gatgaaagac	aaagacggaa	aagagtatca	6120
aaggcagaaa	ggagatcatt	tagttgggtc	tgaaaggaaa	agtntttgct	atccgacatg	6180
tactgctagt	wcctgtaagc	attttaggtc	ccagaatgga	aaaaaaaatc	aagctatngg	6240
ttatataata	atgnnnnnnn	nnnnnnnnnn	nntcgagcat	gcatctagag	ggccctattc	6300
tatagtgtca	cctaaatgct	agagctcgct	gatcagcctc	gactgtgcct	tctagttgcc	6360
agccatctgt	tgtttgcccc	tcccccgctg	cttccttgac	cctggaagggt	gccactccca	6420
ctgtcctttc	ctaataaaa	gaggaaattg	catcgcattg	tctgagtagg	tgtcattcta	6480
ttctgggggg	tggggtgggg	caggacagca	agggggagga	ttgggaagac	aatagcaggc	6540
atgctgggga	tgcggtgggc	tctatggctt	ctgaggcgga	aagaaccagc	tggggctcta	6600
gggggtatcc	ccacgcgccc	tgtagcggcg	cattaagcgc	ggcgggtgtg	gtgggttacgc	6660
gcagcgtgac	cgctacactt	gccagcgccc	tagcgcggcg	tcctttcgct	ttcttccctt	6720
cctttctcgc	cacgttcgcc	ggctttcccc	gtcaagctct	aaatcggggc	atccctttag	6780
ggttcgatt	tagtgcttta	cggcacctcg	accccaaaaa	acttgattag	ggtgatgggt	6840
cacgtagtgg	gccatcgccc	tgatagacgg	tttttcgccc	tttgacgttg	gagtccacgt	6900



tctttaatag	tggactcttg	ttccaaactg	gaacaacact	caaccctatc	tcggtctatt	6960
cttttgattt	ataagggatt	ttgggggattt	cggcctattg	gttaaaaaat	gagctgattt	7020
aacaaaaatt	taacgcgaat	tctagagccc	cgccgcccga	cgaactaaac	ctgactacgg	7080
catctctgcc	ccttcttcgc	ggggcagtg	atgtaatccc	ttcagttggg	tggtaacaact	7140
tgccaactgg	gccctgttcc	acatgtgaca	cgggggggga	ccaaacacaa	aggggttctc	7200
tgactgtagt	tgacatcctt	ataaatggat	gtgcacattt	gccaacactg	agtggctttc	7260
atcctggagc	agactttgca	gtctgtggac	tgcaacacaa	cattgccttt	atgtgtaact	7320
cttggtgaa	gctcttacac	caatgctggg	ggacatgtac	ctcccagggg	cccaggaaga	7380
ctacgggagg	ctacaccaac	gtcaatcaga	ggggcctgtg	tagctaccga	taagcggacc	7440
ctcaagaggg	cattagcaat	agtgtttata	aggccccctt	gttaacccta	aacgggtagc	7500
atatgcttcc	cgggtagtag	tatatactat	ccagactaac	cctaattcaa	tagcatatgt	7560
taccaacgg	gaagcatatg	ctatcgaatt	agggtagta	aaagggtcct	aaggaacagc	7620
gatatctccc	accccatgag	ctgtcacggg	tttatttaca	tggggtcagg	attccacgag	7680
ggtagtgaac	catttttagtc	acaagggcag	tggctgaaga	tcaaggagcg	ggcagtgaac	7740
tctcctgaat	cttcgcctgc	ttcttcattc	tccttcgttt	agctaataga	ataactgctg	7800
agttgtgaac	agtaagggtg	atgtgaggtg	ctcgaaaaca	aggttttcagg	tgacgcccc	7860
agaataaaa	ttggacgggg	ggttcagtg	tggcattgtg	ctatgacacc	aatataaccc	7920
tcacaaaccc	cttgggcaat	aaatactagt	gtaggaatga	aacattctga	atatctttta	7980
caatagaaa	ccatgggggtg	gggacaagcc	gtaaagactg	gatgtccatc	tcacacgaat	8040
ttatggctat	gggcaacaca	taatcctagt	gcaatatgat	actgggggta	ttaagatgtg	8100
tcccaggcag	ggaccaagac	aggtgaacca	tgttgttaca	ctctattttgt	aacaagggga	8160
aagagagtgg	acgccgacag	cagcggactc	cactggttgt	ctctaacacc	ccgaaaaatt	8220
aaacggggct	ccacgccaat	ggggcccata	aacaaagaca	agtggccact	cttttttttg	8280
aaattgtgga	gtgggggcac	gcgtcagccc	ccacacgccg	ccctgcgggt	ttggactgta	8340
aaataagggt	gtaataactt	ggctgattgt	aaccccgcct	accactgcgg	tcaaaccact	8400
tgcccacaaa	accactaatg	gcaccccggg	gaataacctgc	ataagtaggt	gggcggggcca	8460
agataggggc	gcgattgctg	cgatctggag	gacaaattac	acacacttgc	gcctgagcgc	8520
caagcacagg	gttgttggtc	ctcatattca	cgaggctcgt	gagagcacgg	tgggctaata	8580
ttgccatggg	tagcatatac	tacccaaata	tctgtagatg	atatgctatc	ctaatactata	8640
tctgggtagc	ataggctatc	ctaattctata	tctgggtagc	atatgctatc	ctaattctata	8700
tctgggtagt	atatgctatc	ctaatttata	tctgggtagc	ataggctatc	ctaattctata	8760
tctgggtagc	atatgctatc	ctaattctata	tctgggtagt	atatgctatc	ctaattctgta	8820
tccgggtagc	atatgctatc	ctaattagaga	ttagggtagt	atatgctatc	ctaatttata	8880
tctgggtagc	atatactacc	caaatatctg	gatagcatat	gctatcctaa	tctatatctg	8940
ggtagcatat	gctatcctaa	tctatatctg	ggtagcatag	gctatcctaa	tctatatctg	9000
ggtagcatat	gctatcctaa	tctatatctg	ggtagtatat	gctatcctaa	tttatatctg	9060
ggtagtatat	gctatcctaa	tctgtatccg	ggtagcatat	gctatcctaa	tctatatctg	9120
gtcagcatat	gatacccgat	agtagagtgg	gagtgtctatc	ctttgcataat	gccgccacct	9180
cccaaggggg	cgtgaatttt	cgctgcttgt	ccttttcctg	catgctgggt	gctcccatct	9240
ttaggtgaat	ttaaggaggc	caggctaaag	ccgtcgcagt	tctgattgct	caccaggtaa	9300
atgtcgctaa	tgttttccaa	cgcgagaagg	tggtgagcgc	ggagctgagt	gacgtgacaa	9360
catgggtatg	cccaattgcc	ccatgttggg	aggacgaaaa	tggtgacaag	acagatggcc	9420
agaaatacac	caacagcacg	catgatgtct	actggggatt	tattcttttag	tgcgggggaa	9480
tacacggctt	ttaatacgat	tgagggcgct	tcctaacaag	ttacatcact	cctgcctctc	9540
ctcacccctc	tctccatcac	ctccttcac	tcctgcactc	ccgtcatcac	cctccgcggc	9600
agcccccttc	accatagggtg	gaaaccaggg	aggcaaatct	actccatcgt	caaagctgca	9660
cacagtcacc	ctgatattgc	aggtaggagc	gggctttgtc	ataacaagg	ccttaatcgc	9720
atccttcaaa	acctcagcaa	atatatgagt	ttgtaaaaag	accatgaaat	aacagacaat	9780
ggactccctt	agcgggccag	gttgtgggccc	gggtccaggg	gccattccaa	aggggagacg	9840
actcaatggg	gtaagacgac	attgtggaat	agcaagggca	gttcctcgcc	ttaggttgta	9900
aaggggaggtc	ttactacctc	catatacgaa	cacaccggcg	acccaagtgc	cttcgtcggt	9960
agtcctttct	acgtgactcc	tagccaggag	agctcttaaa	ccttctgcaa	tggttctcaa	10020
tttcgggttg	gaacctcctt	gaccacgatg	ctttccaaac	cacctcctt	ttttgcgcct	10080
gcctccatca	ccctgacccc	ggggtcacgt	gcttgggcct	tctcctgggt	catctgcggg	10140
gcctcgctct	atcgctcccg	ggggcacgtc	aggctacca	tctggggccac	cttcttggtg	10200
gtattcaaaa	taatcggtct	cccctacagg	gtggaaaaat	ggccttctac	ctggaggggg	10260
cctgcgcggg	ggagaccggg	atgatgatga	ctgactactg	ggactcctgg	gcctcttttc	10320
tccacgtcca	cgacctctcc	ccctggctct	ttcacgactt	ccccccctgg	ctctttcacg	10380
tcctctaccc	cggcggcctc	cactacctcc	tgcaccccg	cctccactac	ctcctcgacc	10440
ccggcctcca	ctgcctcctc	gacccccggc	tccacctcct	gctcctgccc	ctcctgctcc	10500
						10560

tgccccctcct	cctgctcctg	ccccctcctgc	ccctcctgct	cctgccccctc	ctgccccctcc	10620
tgctcctgccc	cctcctgccc	ctcctgctcc	tgccccctcct	gccccctcctc	ctgctcctgc	10680
ccctcctgccc	cctcctcctg	ctcctgcccc	tectgccccct	cctgctcctg	ccccctcctgc	10740
ccctcctgct	cctgccccctc	ctgccccctcc	tgctcctgccc	cctcctgctc	ctgccccctcc	10800
tgctcctgccc	cctcctgctc	ctgccccctcc	tgccccctcct	gccccctcctc	ctgctcctgc	10860
ccctcctgct	cctgccccctc	ctgccccctcc	tgccccctcct	gctcctgccc	ctcctcctgc	10920
tcctgccccct	cctgccccctc	ctgccccctcc	tcctgctcct	gccccctcctg	ccccctcctcc	10980
tgctcctgccc	cctcctcctg	ctcctgcccc	tcctgccccct	cctgccccctc	ctcctgctcc	11040
tgccccctcct	gccccctcctc	ctgctcctgc	ccctcctcct	gctcctgccc	ctcctgcccc	11100
tcctgccccct	cctcctgctc	ctgccccctcc	tcctgctcct	gccccctcctg	ccccctcctgc	11160
ccctcctgccc	ctcctcctcctg	ctcctgcccc	tcctcctgct	cctgccccctc	ctgctcctgc	11220
ccctcccgcct	cctgctcctg	ctcctgttcc	accgtgggtc	cctttgcagc	caatgcaact	11280
tggacgtttt	tgggggtctcc	ggacaccatc	tctatgtctt	ggccctgac	ctgagccgcc	11340
cgggggtcct	ggtcttccgc	ctcctcgtcc	tcgtcctctt	ccccgtcctc	gtccatggtt	11400
atcacccccct	cttcttttgag	gtccactgcc	gccggagcct	tctgggtccag	atgtgtctcc	11460
cttctctcct	aggccatttc	caggctcctgt	acctggcccc	tcgtcagaca	tgattcacac	11520
taaaagagat	caatagacat	ctttattaga	cgacgctcag	tgaatacagg	gagtgcagac	11580
tcctgcccc	tccaacagcc	ccccaccct	catccccctc	atggctcgtg	tcagacagat	11640
ccaggtctga	aaattcccc	tcctccgaac	catcctcgtc	ctcatcacca	attactcgca	11700
gcccggaaaa	ctcccgtga	acatcctcaa	gatttgcgtc	ctgagcctca	agccaggcct	11760
caaatctctc	gtcccccttt	ttgctggacg	gtagggtagg	ggattctcgg	gaccctcct	11820
cttctctctc	aaggtcacca	gacagagatg	ctactggggc	aacggaagaa	aagctgggtg	11880
cggcctgtga	ggatcagctt	atcgatgata	agctgtcaaa	catgagaatt	cttgaagacg	11940
aaagggcctc	gtgatacgcc	tatttttata	ggttaatgtc	atgataataa	tgggtttctta	12000
gacgtcaggt	ggcacttttc	ggggaaatgt	gcgcggaacc	cctattttgtt	tattttttcta	12060
aatacattca	aatatgtatc	cgctcatgag	acaataaccc	tgataaatgc	ttcaataata	12120
ttgaaaaagg	aagagtatga	gtattcaaca	tttccgtgtc	gcccttattc	cctttttttgc	12180
ggcattttgc	cttctgttt	ttgctcacc	agaaacgctg	gtgaaagtaa	aagatgctga	12240
agatcagttg	gtgtcacgag	tgggttacat	cgaactggat	ctcaacagcg	gtaagatcct	12300
tgagagtttt	cgccccgaag	aacgttttcc	aatgatgagc	actttttaaag	ttctgctatg	12360
tggcgcggta	ttatcccgtg	ttgacgccgg	gcaagagcaa	ctcggctcgc	gcatacacta	12420
ttctcagaat	gacttggttg	agtactcacc	agtcacagaa	aagcatctta	cggatggcat	12480
gacagtaaga	gaattatgca	gtgctgccat	aaccatgagt	gataacactg	cggccaactt	12540
acttctgaca	acgatcggag	gaccgaagga	gctaaccgct	tttttgca	acatggggga	12600
tcatgtaact	cgccttgatc	gttgggaacc	ggagctgaat	gaagccatac	caaacgcagca	12660
gcgtgacacc	acgatgcctg	cagcaatggc	aacaacgttg	cgcaaactat	taactggcga	12720
actacttact	ctagcttccc	ggcaacaatt	aatagactgg	atggaggcgg	ataaagttag	12780
aggaccactt	ctgcgctcgg	cccttcggcg	ttgctggttt	attgctgata	aatctggagc	12840
cgggtgagcgt	gggtctcggc	gtatcattgc	agcactgggg	ccagatggta	agccctcccg	12900
tatcgtagtt	atctacacga	cggggagtca	ggcaactatg	gatgaacgaa	atagacagat	12960
cgctgagata	ggtgcctcac	tgattaagca	ttggtaactg	tcagaccaag	tttactcata	13020
tatactttag	attgatttaa	aacttcattt	ttaatttaaa	aggatctagg	tgaagatcct	13080
ttttgataat	ctcatgacca	aaatccctta	acgtgagttt	tcgttccact	gagcgtcaga	13140
ccccgtagaa	aagatcaaag	gatcttcttg	agatectttt	tttctgcggc	taatctgctg	13200
cttgcaaaaca	aaaaaaccac	cgtaccagc	ggtggtttgt	ttgccggatc	aagagctacc	13260
aactcttttt	ccgaaggtaa	ctggcttcag	cagagcgcag	ataccaaata	ctgtccttct	13320
agtgtagctg	tagttaggcc	accacttcaa	gaactctgta	gcaccgccta	catacctcgc	13380
tctgctaatac	ctgttaccag	tggctgctgc	cagtggcgat	aagtcgtgtc	ttaccgggtt	13440
ggactcaaga	cgatagttac	cggataaaggc	gcagcggtcg	ggctgaacgg	ggggttcgtg	13500
cacacagccc	agcttgagc	gaacgacctc	caccgaactg	agatacctac	agcgtgagct	13560
atgagaaaagc	gccacgcttc	ccgaaggag	aaaggcggac	aggatccgg	taagcggcag	13620
ggtcggaaaca	ggagagcgca	cggaggagct	tccaggggga	aacgcctggt	atctttatag	13680
tcctgtcggg	tttcgccacc	tctgacttga	gcgtcgattt	ttgtgatgct	cgtcaggggg	13740
gcggagccta	tggaaaaacg	ccagcaacgc	ggccttttta	cggttcctgg	ccttttgctg	13800
cgccgcgtgc	ggctgctgga	gatggcggac	gcgatggata	tgttctgcca	aggggtggtt	13860
tgcgcatcca	cagttctccg	caagaattga	ttggtcccaa	ttcttgaggt	ggtgaatccg	13920
ttagcgaggt	gccgcggct	tccattcagg	tcgaggtggc	ccggctccat	gcaccgcgac	13980
gcaacgcggg	gaggcagaca	aggtataggg	cggcgcctac	aatccatgcc	aaccgcgttc	14040
atgtgctcgc	cgaggcggca	taaatcgccg	tgacgatcag	cggctccagt	atcgaagtta	14100
ggctggttaag	agccgcgagc	gatccttgaa	gctgtccctg	atggctcgta	tctacctgcc	14160
tggacagcat	ggcctgcaac	gcgggcatcc	cgatgccgc	ggaagcgaga	agaatcataa	14220

tggggaaggc	catccagcct	cgcgtcgcga	acgccagcaa	gacgtagccc	agcgcgtcgg	14280
ccgccatgcc	ctgcttcata	cccgtggccc	gttgctcgcg	tttgctggcg	gtgtccccgg	14340
aagaaatata	tttgcattgt	tttagttcta	tgatgacaca	aaccccgccc	agcgtcttgt	14400
cattggcgaa	ttcgaacacg	cagatgcagt	cggggcgggc	cggtcccagg	tccacttcgc	14460
atattaaggt	gacgcgtgtg	gcctcgaaca	ccgagcgacc	ctgcagcgac	ccgcttaaca	14520
gcgtcaacag	cgtgccgcag	atcccgggca	atgagatatg	aaaaagcctg	aactcaccgc	14580
gacgtctgtc	gagaagtttc	tgatcgaaaa	gttcgacagc	gtctccgacc	tgatgcagct	14640
ctcggagggc	gaagaatctc	gtgctttcag	cttcgatgta	ggagggcgtg	gatatgtcct	14700
gcgggtaaat	agctgcgcgc	atggttttcta	caaagatcgt	tagtgggatc	ggcactttgc	14760
atcggccgcg	ctccccgatt	ccggaagtgc	ttgacattgg	ggaattcagc	gagagcctga	14820
cctattgcat	ctccccgcgt	gcacaggggtg	tcacgttgca	agacctgcct	gaaaccgaac	14880
tgcccgcgtg	tctgcagcgc	gtcgcggagg	ccatggatgc	gatcgcgtcg	gccgatctta	14940
gccagacgag	cgggttcggc	ccattcggac	cgcaaggaat	cggtcaatac	actacatggc	15000
gtgatttcat	atgcgcgatt	gctgatcccc	atgtgatca	ctggcaaact	gtgatggacg	15060
acaccgtcag	tgcgtccgtc	gcgcaggctc	tcgatgagct	gatgctttgg	gccgaggact	15120
gccccgaagt	ccggcacctc	gtgcacgcgg	atttcggctc	caacaatgtc	ctgacggaca	15180
atggccgcat	aacagcggtc	attgactgga	gcgaggcgat	gttcggggat	tcccaatacg	15240
aggtcgccaa	catctttctc	tggaggccgt	ggttgccggg	tatggagcag	cagacgcgct	15300
acttcgagcg	gaggcattcc	gagcttgca	gatcgccgcg	gctccggggc	tatatgctcc	15360
gcattggctc	tgaccaactc	tatcagagct	tggttgacgg	caatttcgat	gatgcagctt	15420
ggg'gcgagg	tcgatgcgac	gcaatcgtcc	gatccggagc	cgggactgtc	gggcgtacac	15480
aaatcgcccc	cagaagcgcg	gccgtctgga	ccgatggctg	tgtagaagta	ctcgccgata	15540
gtggaaacgg	gagatggggg	aggctaactg	aaacacggaa	ggagacaata	ccggaaggaa	15600
cccgcgctat	gacggcaata	aaaagacaga	ataaaaacga	cgggtgttgg	gtcgtttgtt	15660
cataaacgcg	gggttcggtc	ccagggtctg	cactctgtcg	ataccccacc	gagaccccat	15720
tggggccaat	acgcccgcg	ttcttctctt	tccccacccc	accccccaag	ttcgggtgaa	15780
ggcccagggc	tcgcagccaa	cgtcggggcg	gcaggccctg	ccatagccac	tggccccgtg	15840
ggttaggagc	ggggtccccc	atggggaatg	gtttatgggt	cgtggggggt	attattttgg	15900
gcgttgcggtg	gggtctgtgc	cacgactgga	ctgagcagac	agacccatgg	tttttggatg	15960
gcctgggcat	ggaccgcatt	taactggcg	acacgaacac	cgggcgtctg	tggctgccaa	16020
acacccccga	cccccaaaaa	ccaccgcgcg	gatttctggc	gtgccaagct	agtcgaccaa	16080

<210> 49  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 cccggccgga ggggcagctt tgtggagatg gt

32

<210> 50  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
 1 5 10

<210> 51  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 51  
 Val Asn Leu Asp Ala  
 1 5

<210> 52  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic oligopeptide substrate

<400> 52  
Ser Glu Val Asn Leu Asp Ala Glu Phe  
1 5

<210> 53  
<211> 30  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic oligopeptide substrate

<400> 53  
Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile  
1 5 10 15  
Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe  
20 25 30

<210> 54  
<211> 5  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Wild type Amyloid Precursor Protein cleavage site  
(fragment)

<400> 54  
Val Lys Met Asp Ala  
1 5

<210> 55  
<211> 24  
<212> PRT  
<213> Homo sapiens

<400> 55  
Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val  
1 5 10 15  
Glu Met Val Asp Asn Leu Arg Gly  
20

<210> 56  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 56  
Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg  
1 5 10 15

<210> 57  
<211> 419

<212> PRT

<213> Homo sapiens

<400> 57

```
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1          5          10          15
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
          20          25          30
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
          35          40          45
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
          50          55          60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65          70          75          80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
          85          90          95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
          100          105          110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
          115          120          125
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
          130          135          140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145          150          155          160
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
          165          170          175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
          180          185          190
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
          195          200          205
Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
          210          215          220
Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225          230          235          240
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
          245          250          255
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
          260          265          270
Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
          275          280          285
Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
          290          295          300
Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305          310          315          320
Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
          325          330          335
Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
          340          345          350
Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
          355          360          365
Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
          370          375          380
Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385          390          395          400
Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
          405          410          415
Val Ser Ala
```

<210> 58

<211> 407

<212> PRT

<213> Homo sapiens

<400> 58

Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	
1				5					10					15		
Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	
			20					25					30			
Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	
		35					40					45				
Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	
	50					55					60					
His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	
65				70						75					80	
Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	
				85					90					95		
Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	
			100					105					110			
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	
		115					120					125				
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	
	130					135					140					
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	
145				150						155					160	
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	
				165					170					175		
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	
			180					185					190			
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	
		195					200					205				
Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	
	210					215					220					
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	
225				230						235					240	
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	
				245					250					255		
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	
			260					265					270			
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	
			275					280					285			
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	
	290					295					300					
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	
305				310						315					320	
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	
				325					330					335		
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	
			340					345					350			
Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	
	355						360					365				
Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	
	370					375					380					
Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	
385				390						395					400	
Asn	Ile	Pro	Gln	Thr	Asp	Glu										
				405												

<210> 59

<211> 452

<212> PRT

<213> Homo sapiens

<400> 59

```

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1      5      10      15
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
      20      25      30
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
      35      40      45
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
      50      55      60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65      70      75      80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
      85      90      95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
      100     105     110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
      115     120     125
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
      130     135     140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145     150     155     160
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
      165     170     175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
      180     185     190
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
      195     200     205
Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
      210     215     220
Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225     230     235     240
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
      245     250     255
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
      260     265     270
Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
      275     280     285
Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
      290     295     300
Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305     310     315     320
Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
      325     330     335
Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
      340     345     350
Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
      355     360     365
Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
      370     375     380
Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385     390     395     400
Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
      405     410     415
Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
      420     425     430
Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
      435     440     445
Gln Thr Asp Glu
      450

```

<210> 60  
 <211> 420  
 <212> PRT  
 <213> Homo sapiens

<400> 60  
 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
 1 5 10 15  
 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
 20 25 30  
 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
 35 40 45  
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
 50 55 60  
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
 65 70 75 80  
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
 85 90 95  
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
 100 105 110  
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
 115 120 125  
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
 130 135 140  
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
 145 150 155 160  
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
 165 170 175  
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
 180 185 190  
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
 195 200 205  
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
 210 215 220  
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
 225 230 235 240  
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
 245 250 255  
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
 260 265 270  
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
 275 280 285  
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
 290 295 300  
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
 305 310 315 320  
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
 325 330 335  
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
 340 345 350  
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
 355 360 365  
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
 370 375 380  
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
 385 390 395 400  
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
 405 410 415  
 Val Ser Ala Cys  
 420



<210> 61  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic peptide inhibitor  
  
 <220>  
 <221> MOD\_RES  
 <222> 4  
 <223> Xaa = hydroxyethylene  
  
 <400> 61  
 Glu Val Met Xaa Ala Glu Phe  
 1 5  
  
 <210> 62  
 <211> 26  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 62  
 Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met  
 1 5 10 15  
 Leu Pro Leu Cys Leu Met Val Cys Gln Trp  
 20 25  
  
 <210> 63  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> P26-P4'sw peptide substrate  
  
 <400> 63  
 Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu  
 1 5 10 15  
 Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu  
 20 25 30  
 Phe  
  
 <210> 64  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> P26-P1' peptide substrate with CGG linker  
  
 <400> 64  
 Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu  
 1 5 10 15  
 Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu  
 20 25  
  
 <210> 65  
 <211> 501

<212> PRT

<213> Mus musculus

<400> 65

Met	Ala	Pro	Ala	Leu	His	Trp	Leu	Leu	Leu	Trp	Val	Gly	Ser	Gly	Met
1				5					10					15	
Leu	Pro	Ala	Gln	Gly	Thr	His	Leu	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
			20					25					30		
Gly	Leu	Ala	Gly	Pro	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			
Glu	Glu	Ser	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70					75					80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
			100					105					110		
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
		115					120					125			
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130					135					140				
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145					150					155					160
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
				165					170					175	
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
			180					185					190		
Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Ile	Pro
		195					200					205			
Asn	Ile	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln
	210					215					220				
Thr	Glu	Ala	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile
225					230					235					240
Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg
			245						250					255	
Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln
			260					265					270		
Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val
		275					280					285			
Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala
	290					295					300				
Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp
305					310					315					320
Gly	Phe	Trp	Leu	Gly	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	
				325				330					335		
Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val
			340					345					350		
Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg
		355					360					365			
Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala
	370					375					380				
Val	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu
385					390					395					400
Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala
				405					410					415	
Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu
			420					425					430		
Gly	Pro	Phe	Val	Thr	Ala	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro
		435					440						445		

Gln	Thr	Asp	Glu	Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	
	450					455					460					
Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	
465					470					475					480	
Arg	Cys	Leu	Arg	Cys	Leu	Arg	His	Gln	His	Asp	Asp	Phe	Gly	Asp	Asp	
				485					490					495		
Ile	Ser	Leu	Leu	Lys												
			500													

<210> 66  
 <211> 480  
 <212> PRT  
 <213> Homo sapiens

<400> 66

Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser	Gly	Leu	Gly	Gly	Ala	
1				5					10					15		
Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	
			20					25					30			
Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	
			35				40					45				
Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	
	50					55					60					
Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	
65					70					75					80	
Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	
				85					90					95		
Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	
			100					105					110			
Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	
		115				120						125				
His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	
	130					135					140					
Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	
145					150					155					160	
Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	
				165					170					175		
Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	
			180					185					190			
Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	
		195					200					205				
Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	
	210				215						220					
Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	
225					230					235					240	
Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	
				245					250					255		
Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	
			260					265					270			
Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	
		275					280					285				
Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	
	290					295					300					
Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	
305					310					315					320	
Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	
				325					330					335		
Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	
			340					345					350			
Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	
		355					360					365				

Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val
	370					375					380				
Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His
385					390					395					400
Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr
				405					410					415	
Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser
			420					425					430		
Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu	Phe
		435					440					445			
Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg	Cys
	450					455					460				
Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser	Leu	Leu	Lys
465					470					475					480

<210> 67

<211> 444

<212> PRT

<213> Homo sapiens

<400> 67

Gly	Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln
1				5					10					15	
Gly	Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn
			20					25					30		
Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro
		35					40					45			
His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr
	50					55					60				
Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp
65				70					75						80
Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn
				85					90					95	
Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe
			100					105					110		
Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala
		115					120					125			
Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu
	130				135						140				
Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly
145				150					155						160
Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly
			165						170					175	
Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu
			180					185					190		
Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val
		195					200					205			
Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr
	210				215						220				
Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu
225					230					235					240
Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser
			245						250					255	
Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val
		260					265						270		
Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser
		275				280						285			
Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile
290						295					300				

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
 305 310 315 320  
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
 325 330 335  
 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
 340 345 350  
 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
 355 360 365  
 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
 370 375 380  
 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr  
 385 390 395 400  
 Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu  
  
 405 410 415  
 Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln  
 420 425 430  
 His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys  
 435 440

<210> 68  
 <211> 395  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln  
 1 5 10 15  
 Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn  
 20 25 30  
 Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro  
 35 40 45  
 His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr  
 50 55 60  
 Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp  
 65 70 75 80  
 Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn  
 85 90 95  
 Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe  
 100 105 110  
 Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala  
 115 120 125  
 Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu  
 130 135 140  
 Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly  
 145 150 155 160  
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
 165 170 175  
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
 180 185 190  
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
 195 200 205  
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
 210 215 220  
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
 225 230 235 240  
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
 245 250 255  
 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
 260 265 270

Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser
		275					280					285			
Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile
	290					295					300				
Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln
305				310						315					320
Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val
			325						330					335	
Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala
		340						345					350		
Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu
		355					360					365			
Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu
	370					375					380				
Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu					
385					390					395					

<210> 69

<211> 439

<212> PRT

<213> Homo sapiens

<400> 69

Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu
1				5					10					15	
Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr
			20					25					30		
Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His
		35					40					45			
Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys
	50					55					60				
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly
65					70					75				80	
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala
				85					90					95	
Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser
			100					105					110		
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro
		115				120						125			
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His
	130					135					140				
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu
145					150					155					160
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly
				165					170					175	
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile
			180					185					190		
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn
		195					200					205			
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser
	210					215					220				
Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe
225					230						235				240
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe
				245					250					255	
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly
			260					265					270		
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly
		275					280					285			
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr
	290					295					300				

Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys
305					310					315					320
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile
				325					330						335
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly
			340					345					350		
Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala
		355					360					365			
Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn
	370					375					380				
Ile	Pro	Gln	Thr	Asp	Glu	Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met
385					390					395					400
Ala	Ala	Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys
			405						410						415
Gln	Trp	Arg	Cys	Leu	Arg	Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala
			420					425					430		
Asp	Asp	Ile	Ser	Leu	Leu	Lys									
		435													

<210> 70

<211> 390

<212> PRT

<213> Homo sapiens

<400> 70

Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu
1				5					10					15	
Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr
			20					25					30		
Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His
		35					40					45			
Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys
	50					55					60				
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly
65					70					75					80
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala
				85					90					95	
Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser
			100					105					110		
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro
		115					120					125			
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His
	130					135					140				
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu
145					150					155					160
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly
			165						170					175	
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile
			180					185						190	
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn
		195					200					205			
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser
	210					215					220				
Ile	Val	Asp	Ser	Gly	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	
225					230				235						240
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe
			245						250					255	
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly
			260					265					270		
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly
		275					280					285			

Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr
290						295					300				
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys
305				310						315					320
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile
			325					330						335	
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly
			340					345					350		
Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala
		355					360					365			
Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn
370						375					380				
Ile	Pro	Gln	Thr	Asp	Glu										
385					390										

<210> 71

<211> 374

<212> PRT

<213> Homo sapiens

<400> 71

Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val
1				5					10					15	
Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val
			20					25					30		
Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp
		35					40					45			
Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu
50					55						60				
His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg
65				70						75					80
Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu
			85						90					95	
Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg
		100						105					110		
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly
		115					120					125			
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg
		130				135					140				
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr
145				150						155					160
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro
			165						170					175	
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile
			180					185					190		
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro
		195					200					205			
Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile
	210					215					220				
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys
225				230						235					240
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val
			245						250					255	
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys
		260						265					270		
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala
		275					280					285			
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met
	290					295					300				
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln
305					310					315					320





Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	100	105	110
Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	115	120	125
His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	130	135	140
Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	145	150	155
Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	165	170	175
Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	180	185	190
Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	195	200	205
Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	210	215	220
Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	225	230	235
Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	245	250	255
Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	260	265	270
Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	275	280	285
Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	290	295	300
Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	305	310	315
Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	325	330	335
Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	340	345	350
Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	355	360	365
Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	370	375	380
Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His	385	390	395
Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	405	410	415
Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu		420	425	430

<210> 75

<211> 361

<212> PRT

<213> Homo sapiens

<400> 75

Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	1	5	10	15
Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	20	25	30	35
Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	40	45	50	55
Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	60	65	70	75
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	80	85	90	95
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala				

Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	
			100					105					110			
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	
		115					120					125				
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	
		130				135					140					
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	
145					150					155					160	
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	
			165						170					175		
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	
		180						185					190			
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	
		195				200						205				
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	
	210				215						220					
Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	
225					230					235					240	
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	
			245					250						255		
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	
		260					265						270			
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	
		275				280						285				
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	
	290				295						300					
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	
305					310					315					320	
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	
			325					330						335		
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	
		340					345						350			
Phe	Ala	Val	Ser	Ala	Cys	His	Val	His								
		355					360									

<210> 76  
 <211> 63  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(63)  
 <223> n = A,T,C or G

<400> 76  
 garacngayg argarccnga rgarccnggn mgnmgnggnw snttygtnga ratggtn gay  
 aay

60  
 63

<210> 77  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 77  
 Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val  
 1 5 10 15  
 Glu Met Val Asp Asn  
 20

<210> 78

<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Peptide inhibitor P3-P4' XD-V

<220>  
<221> MOD\_RES  
<222> 3  
<223> Xaa is hydroxyethylene or statine

<400> 78  
Val Met Xaa Val Ala Glu Phe  
1 5

<210> 79  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 79  
Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val  
1 5 10

<210> 80  
<211> 419  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> nucleotide insert in vector pCF

<400> 80  
ctggttgggct cgcggttgag gacaaactct tcgcggtcct tccagtactc ttggatcgga 60  
aaccgcgtcgg cctccgaacg gtactccgcc accgagggac ctgagcgagt ccgcatcgac 120  
cggatcggaa aacctctcga ctggtggggt gactactccc tctcaaaagc gggcatgact 180  
tctgcgctaa gattgtcagt ttccaaaaaac gaggaggatt tgatattcac ctggcccgcg 240  
gtgatgcctt tgagggtggc cgcgtccatc tggtcagaaa agacaatctt tttgttgtca 300  
agcttgaggt gtggcaggct tgagatctgg ccatacactt gagtgacaat gacatccact 360  
ttgcctttct ctccacaggt gtccactccc aggtccaact gcaggtcgac tctagaccc 419

<210> 81  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Peptide inhibitor P4-P4' XD-V

<220>  
<221> MOD\_RES  
<222> 4  
<223> Xaa is hydroxyethylene or statine

<400> 81  
Glu Val Met Xaa Val Ala Glu Phe  
1 5

<210> 82

```

<211> 9
<212> PRT
<213> Homo sapiens

<220>

<223> APP fragment P5-P4' wt

<400> 82
Ser Glu Val Lys Met Asp Ala Glu Phe
1          5

<210> 83
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> APP fragment P5-P4'wt

<400> 83
Ser Glu Val Asn Leu Asp Ala Glu Phe
1          5

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 84
Ser Glu Val Lys Leu Asp Ala Glu Phe
1          5

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 85
Ser Glu Val Lys Phe Asp Ala Glu Phe
1          5

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 86
Ser Glu Val Asn Phe Asp Ala Glu Phe
1          5

<210> 87

```

<211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 87  
 Ser Glu Val Lys Met Ala Ala Glu Phe  
 1 5  
  
 <210> 88  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 88  
 Ser Glu Val Asn Leu Ala Ala Glu Phe  
 1 5  
  
 <210> 89  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 89  
 Ser Glu Val Lys Leu Ala Ala Glu Phe  
 1 5  
  
 <210> 90  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 90  
 Ser Glu Val Lys Met Leu Ala Glu Phe  
 1 5  
  
 <210> 91  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 91  
 Ser Glu Val Asn Leu Leu Ala Glu Phe  
 1 5  
  
 <210> 92  
 <211> 9

<212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 92  
 Ser Glu Val Lys Leu Leu Ala Glu Phe  
 1 5  
  
 <210> 93  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 93  
 Ser Glu Val Lys Phe Ala Ala Glu Phe  
 1 5  
  
 <210> 94  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 94  
 Ser Glu Val Asn Phe Ala Ala Glu Phe  
 1 5  
  
 <210> 95  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 95  
 Ser Glu Val Lys Phe Leu Ala Glu Phe  
 1 5  
  
 <210> 96  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> APP fragment  
  
 <400> 96  
 Ser Glu Val Asn Phe Leu Ala Glu Phe  
 1 5  
  
 <210> 97  
 <211> 14  
 <212> PRT

<213> Artificial Sequence

<220>

<223> APP-derived fragment P10-P4' (D-V)

<400> 97

Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Val Ala Glu Phe  
1 5 10

<210> 98

<211> 35

<212> DNA

<213> Homo sapiens

<400> 98

cccgaagagc ccggccggag gggcagcttt gtcga

35

<210> 99

<211> 11

<212> PRT

<213> Homo sapiens

<400> 99

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg  
1 5 10

<210> 100

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant 293T cells

<400> 100

Thr Gln His Gly Ile Arg Leu Pro Leu Arg  
1 5 10

<210> 101

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant 293T cells

<400> 101

Met Val Asp Asn Leu Arg Gly Lys Ser  
1 5

<210> 102

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant CosA2 cells

<400> 102

Gly Ser Phe Val Glu Met Val Asp Asn Leu  
1 5 10



<210> 103  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> APP substrate fragment:WT Sequence

<400> 103  
Val Lys Met Asp  
1

<210> 104  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> APP substrate fragment:Swedish Sequence

<400> 104  
Val Asn Leu Asp  
1